

OY 32 DROEYECCKROCMOLETSGOMR-CVSOCCKRFEEDIDMSK 71

RESULT 2

ID VCLA.GOSHI STANDARD; PRT; 605 AA.

AC P09799;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).

OS Gossypium hirsutum (Upland cotton).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium. [1]

RN SEQUENCE FROM N.A.

RA Chlan C.A., Borroto K., Kamalay J.A., Dure L. III;

RT "Developmental biochemistry of cottonseed embryogenesis and germination. XIX. Sequences and genomic organization of the alpha globulin (VICILIN) genes of cottonseed.";

RL Plant Mol. Biol. 9:533-546(1987).

CC -1- FUNCTION: SEED STORAGE PROTEIN.

CC -1- SUBCELLULAR LOCATION: COTYLEDONARY MEMBRANE-BOUND VACUOLAR PROTEIN BODIES.

CC -1- SIMILARITY: TO OTHER 7S SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVULCIN, CONGLICININ, ETC.).

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CC

DR EMBL: M19378: AAA33069.1; -

DR PIR: S06398; S06398.

DR HSSP: P50477: ICAX.

DR PRAM: PF00546; Seedstore_7s; 1.

KW Seed storage protein; Signal.

FT SIGNAL 1 23

FT CHAIN 24 605 VICILIN GC72-A.

SO SEQUENCE 605 AA; 71049 MW; C9DB9371C976953B CRC64;

Query Match 28.0%; Score 101; DB 1; Length 605;

Best Local Similarity 39.0%; Pred. No. 1.36e-05;

Matches 16; Conservative 12; Mismatches 9; Indels 4; Gaps 4;

DB 33 SEDDP00RYEDCKRC-OLETRGOTBEDCKEDRSETOLKEE 72

OY 29 SEDPDRQ-YECKRCQCMOLETSGOM-R-RCVSQCKDRFEED 66

RESULT 3

ID AGRP.LUCFY STANDARD; PRT; 47 AA.

AC P56568;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE 6.5 KD ARGININE/GLUTAMATE-RICH POLYPEPTIDE (6.5K-AGRP).

OS Lufla cylindrica (Smooth loofah) (Sponge gourd).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Lufla. [1]

RN SEQUENCE.

RC TISSUE-SEED.

RX MEDLINE: 97357433.

RA Kimura M., Park S.S., Sakai R., Yamasaki N., Funatsu G.;

RT "Primary structure of 6.5K-arginine/glutamate-rich polypeptide from the seeds of sponge gourd (Lufla cylindrica).";

RL Biosci. Biotechnol. Biochem. 61:984-988(1997).

CC -1- FUNCTION: STORAGE PROTEIN WHICH PROVIDES NITROGEN AND CARBON RESERVES DURING GERMINATION AND SEEDLING GROWTH.

CC -1- MASS SPECTROMETRY: MW=5693.39; METHOD=MALDI.

CC -1- SIMILARITY: SOME, TO 7S SEED STORAGE PROTEINS.

KW Seed storage protein.

FT DISULFID 12 33

FT DISULFID 16 29

SO SEQUENCE 47 AA; 5698 MW; 588B0EC82273AC05 CRC64;

Query Match 27.7%; Score 100; DB 1; Length 47;

Best Local Similarity 41.2%; Pred. No. 2.12e-05;

Matches 14; Conservative 6; Mismatches 13; Indels 1; Gaps 1;

DB 6 RTYEACRVRCQVAEHGVEBRRRCQVCEKRLRE 39

OY 33 ROEYECCKROCMOLETSGOM-RCVSCCKRFEED 65

RESULT 4

ID TSP1.HUMAN STANDARD; PRT; 1170 AA.

AC P07996;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE THROMBOSPONDIN 1 PRECURSOR.

GN THBS1 OR TSP1 OR TSP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. [1]

RN SEQUENCE FROM N.A.

RC TISSUE-ENDOTHELIAL CELLS.

RX MEDLINE: 87057617.

RA Lawler J., Hynes R.O.;

RT "The structure of human thrombospondin, an adhesive glycoprotein with multiple calcium-binding sites and homologs with several different proteins.";

RT 5. Cell Biol. 103:1635-1648(1986).

RN

RL

RN SEQUENCE FROM N.A.

RP MEDLINE: 89133950.

RX Hennessy S.W., Frazier B.A., Kim D.D., Deckwerth T.L.,

RA Baungartel D.M., Rotwein P., Frazier W.A.;

RT "Complete thrombospondin mRNA sequence includes potential regulatory sites in the 3' untranslated region.";

RL J. Cell Biol. 108:729-736(1989).

RN

RP SEQUENCE OF 1-397 FROM N.A.

RX MEDLINE: 87157592.

RA Kobayashi S., Eden-McCutchan F., Franson P., Bornstein P.;

RT "Partial amino acid sequence of human thrombospondin as determined by analysis of cDNA clones: homology to malarial circumsporozoite proteins.";

RT Biochemistry 25:8418-8425(1986).

RN

RL

RN SEQUENCE OF 1-374 FROM N.A.

RP MEDLINE: 86287276.

RX Dixit V.M., Hennessy S.W., Grant G.A., Rotwein P., Frazier W.A.;

RT "Characterization of a cDNA encoding the heparin and collagen binding domains of human thrombospondin.";

RL Proc. Natl. Acad. Sci. U.S.A. 83:5449-5453(1986).

RN

RL

RN SEQUENCE OF 1-166 FROM N.A.

RP MEDLINE: 89291870.

RA Laherty C.D., Gierman T.M., Dixit V.M.;

RT "Characterization of the promoter region of the human thrombospondin gene. DNA sequences within the first intron increase transcription.";

RL J. Biol. Chem. 264:11222-11227(1989).

RN

RL

RN SEQUENCE OF 1028-1170 FROM N.A.

RP la Fleur M., Jobin C., Gauthier J., Kreis C.G.;

RT Submitted (XXX-1992) to the EMBL/Genbank/DBJ databases.

RL

CC -1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND

CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN.

-1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.

-1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.

-1- SIMILARITY: CONTAINS 1 WFCC DOMAIN.

-1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.

-1- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS (WHICH BIND CALCIUM).

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EMBL: M25631; AAA36741.1; -
 EMBL: X04685; CAA28370.1; -
 EMBL: X14787; CAA32889.1; -
 EMBL: J04835; AAA61178.1; -
 EMBL: M99425; AAB59366.1; -
 PIR: A05172; A05172.
 PIR: A25812; A25812.
 PIR: A26155; A26155.
 PIR: A30140; A30140.
 PIR: A34274; A34274.
 HSP: P35555; 1EMO.
 MIM: 188060; -
 PROSITE: PS00022; EGF_1; FALSE_NEG.
 PROSITE: PS01186; EGF_2; 1.
 PROSITE: PS01208; WFCC; 1.
 PFM: PF00008; EGF; 2.
 PFM: PF00090; TSP_1; 3.
 PFM: PF00093; wvc; 1.
 Glycoprotein: Cell adhesion; Calcium-binding; Heparin-binding; Repeat: EGF-like domain; Signal.

FT CHAIN 1 18
 FT DOMAIN 19 1170 THROMBOSPONDIN 1.
 FT DOMAIN 19 232 HEPARIN-BINDING (POTENTIAL).
 FT DOMAIN 316 373 WFCC.
 FT DOMAIN 379 548 3 X TSP TYPE-1 REPEATS (CS-LIKE).
 FT DOMAIN 549 690 3 X EGF-TYPE REPEATS.
 FT DOMAIN 723 950 7 X TSP TYPE-3 REPEATS (CA-BINDING).
 FT DOMAIN 951 1170 C-TERMINAL.
 FT REPEAT 379 430 TSP TYPE-1 1.
 FT REPEAT 435 491 TSP TYPE-1 2.
 FT REPEAT 492 548 TSP TYPE-1 3.
 FT DOMAIN 549 587 EGF-LIKE 1.
 FT DOMAIN 588 645 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 646 690 EGF-LIKE 3.
 FT REPEAT 723 758 TSP TYPE-3 1.
 FT REPEAT 759 781 TSP TYPE-3 2.
 FT REPEAT 782 817 TSP TYPE-3 3.
 FT REPEAT 818 840 TSP TYPE-3 4.
 FT REPEAT 841 878 TSP TYPE-3 5.
 FT REPEAT 879 914 TSP TYPE-3 6.
 FT REPEAT 915 950 TSP TYPE-3 7.
 FT SITE 926 928 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 270 270 INTERCHAIN (PROBABLE).
 FT DISULFID 274 274 INTERCHAIN (PROBABLE).
 FT DISULFID 551 562 BY SIMILARITY.
 FT DISULFID 556 572 BY SIMILARITY.
 FT DISULFID 575 586 BY SIMILARITY.
 FT DISULFID 592 608 BY SIMILARITY.
 FT DISULFID 599 617 BY SIMILARITY.
 FT DISULFID 620 644 BY SIMILARITY.
 FT DISULFID 650 663 BY SIMILARITY.
 FT DISULFID 657 676 BY SIMILARITY.
 FT DISULFID 678 689 BY SIMILARITY.
 FT CARBOHYD 248 248 BY SIMILARITY.
 FT CARBOHYD 360 360 POTENTIAL.
 FT CARBOHYD 708 708 POTENTIAL.

FT CARBOHYD 1067 1067 POTENTIAL.
 FT CONFLICT 84 84 T -> A (IN REF. 2, 3 AND 4).
 FT CONFLICT 523 523 T -> A (IN REF. 2).
 SQ SEQUENCE 1170 AA; 129412 MW; 69B3EDE5A3A95E CRC64;

Query Match 26.3%; Score 95; DB 1; Length 1170;
 Best Local Similarity 50.0%; Pred. No. 1,90e-04;
 Matches 12; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

DB 416 SSVORTCHIDECKRFKODGWS 439
 QY 48 TSGQMRRC-VSGCKRFEEDIDWS 70

RESULT 5 STANDARD; PRT; 1170 AA.
 AC P35441;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE THROMBOSPONDIN 1 PRECURSOR.
 OS THBS1 OR TSP1.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92128941.
 RA Lawler J., Duquette M., Ferro P., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A.,
 RT "Characterization of the murine thrombospondin gene.";
 RL Genomics 11:587-600(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92147683.
 RA Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seldin M.F.,
 RA Dixit V.M.,
 RT "Characterization of mouse thrombospondin 2 sequence and expression during cell growth and development.";
 RL J. Biol. Chem. 267:3274-3281(1992).
 RN [3]
 RP SEQUENCE OF 1-490 FROM N.A.
 RX MEDLINE: 90375346.
 RA Bornstein P., Afifi D., Devarayalu S., Framson P., Li P.,
 RT "Characterization of the mouse thrombospondin gene and evaluation of the role of the first intron in human gene expression.";
 RL J. Biol. Chem. 265:16691-16698(1990).
 CC -1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN, LAMININ AND TYPE V COLLAGEN.
 CC -1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WFCC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS (WHICH BIND CALCIUM).
 CC -----
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EMBL: M62470; AAA50611.1; -
 EMBL: M62450; AAA50611.1; JOINED.
 EMBL: M62451; AAA50611.1; JOINED.
 EMBL: M62452; AAA50611.1; JOINED.
 EMBL: M62453; AAA50611.1; JOINED.
 EMBL: M62454; AAA50611.1; JOINED.
 EMBL: M62455; AAA50611.1; JOINED.
 EMBL: M62456; AAA50611.1; JOINED.

FT DISULFID 578 589 BY SIMILARITY.
FT DISULFID 595 611 BY SIMILARITY.
FT DISULFID 602 620 BY SIMILARITY.
FT DISULFID 623 647 BY SIMILARITY.
FT DISULFID 653 666 BY SIMILARITY.
FT DISULFID 660 679 BY SIMILARITY.
FT DISULFID 681 692 BY SIMILARITY.
FT CARBOHYD 155 155 POTENTIAL.
FT CARBOHYD 158 158 POTENTIAL.
FT CARBOHYD 250 250 POTENTIAL.
FT CARBOHYD 363 363 POTENTIAL.
FT CARBOHYD 705 705 POTENTIAL.
FT CARBOHYD 711 711 POTENTIAL.
FT CARBOHYD 1070 1070 POTENTIAL.
SQ SEQUENCE 1173 AA; 130019 MW; A9F036D6516C0F24 CRC64;
Query Match 26.0%; Score 94; DB 1; Length 1173;
Best Local Similarity 50.0%; Pred. No. 2,94e-04;
Matches 12; Conservative 4; Mismatches 7; Indels 1; Gaps 1;
Db 419 SSVQTRSCQIDCDKRFKQDGS 442
QY 48 TSGQMRRC-VGOCCKRFEEDIDMS 70
RESULT 7
ID SBF-SOYBN STANDARD; PRT; 524 AA.
AC 004672;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE SUCROSE-BINDING PROTEIN PRECURSOR (SBP).
GN SBP.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eumphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC glycine.
RN 11
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-50.
RC TISSUE-EMBRYO;
RX MEDLINE; 93104680.
RA Grimes H.D., Overvoorde P.J., Ripp K., Franceschi V.R., Hitz W.D.;
RT "A 62-kD sucrose binding protein is expressed and localized in
tissues actively engaged in sucrose transport.";
RL Plant Cell 4:1561-1574(1992).
CC -1- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
CC -1- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED.
CC -1- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE
MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF
MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.
CC -1- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER
FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
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CC -----
CC EMBL; L06038; AAB03894.1; -
DR PIR; J01730; J01730.
DR HSSP; P50477; ICAM.
DR PFAM; PF00546; Seedstore_7s; 1.
KW Transport; Sugar transport; Signal; Membrane.
FT SIGNAL 1 29

FT CHAIN 30 524 SUCROSE-BINDING PROTEIN.
SQ SEQUENCE 524 AA; 60522 MW; 0251EE90796EF341 CRC64;
Query Match 21.3%; Score 77; DB 1; Length 524;
Best Local Similarity 44.4%; Pred. No. 3.08e-01;
Matches 12; Conservative 6; Mismatches 6; Indels 3; Gaps 2;
Db 43 CKHOCQOQOYTEGKRVCQSCD-RY 68
QY 39 CKRCQMLE-TSGQMRRCVSGCKRF 63
RESULT 8
ID TSP2_HUMAN STANDARD; PRT; 1172 AA.
AC P35442;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE THROMBOSPONDIN 2 PRECURSOR.
GN THBS2 OR TSP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE; 94010892.
RA Labell T.L., Byers P.H.;
RT "Sequence and characterization of the complete human thrombospondin 2
cDNA: potential regulatory role for the 3' untranslated region.";
RL Genomics 17:223-228(1993).
RN 12
RP SEQUENCE OF 560-1172 FROM N.A.
RC TISSUE-FIBROBLAST;
RX MEDLINE; 92217961.
RA Labell T.L., McGockley Milewicz D.J., Distche C.M., Byers P.H.;
RT "Thrombospondin II: partial cDNA sequence, chromosome location, and
expression of a second member of the thrombospondin gene family in
humans.";
RL Genomics 12:421-429(1992).
CC -1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
LAMININ AND TYPE V COLLAGEN.
CC -1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 WFC DOMAIN.
CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS
(WHICH BIND CALCIUM).
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L12350; AAA03703.1; -
DR EMBL; M61339; -; NOT_ANNOTATED_CDS.
DR PIR; A42173; A42173.
DR HSSP; P00740; IIXA.
DR KIM; 188061; -
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01208; WFC; 1.
DR PFAM; PF00008; EGF; 2.
DR PFAM; PF00090; tsp_1; 3.
DR PFAM; PF00093; wfc; 1.
KW Glycoprotein; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
EGF-like domain; Signal.
FT SIGNAL 1 18
FT CHAIN 19 1172
FT DOMAIN 19 232 THROMBOSPONDIN 2.
HEPARIN-BINDING (POTENTIAL).

FT DOMAIN 318 375 WMFC.
 FT DOMAIN 381 548 3 X TSP TYPE-1 REPEATS (CS-LIKE).
 FT DOMAIN 549 692 3 X EGF-TYPE REPEATS.
 FT DOMAIN 725 952 7 X TSP TYPE-3 REPEATS (CA-BINDING).
 FT DOMAIN 953 1172 C-TERMINAL.
 FT REPEAT 381 432 TSP TYPE-1.1.
 FT REPEAT 437 493 TSP TYPE-1.2.
 FT REPEAT 494 548 TSP TYPE-1.3.
 FT DOMAIN 549 589 EGF-LIKE 1.
 FT DOMAIN 590 647 EGF-LIKE 2. CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 648 692 EGF-LIKE 3.
 FT REPEAT 725 760 TSP TYPE-3.1.
 FT REPEAT 761 783 TSP TYPE-3.2.
 FT REPEAT 784 819 TSP TYPE-3.3.
 FT REPEAT 820 842 TSP TYPE-3.4.
 FT REPEAT 843 880 TSP TYPE-3.5.
 FT REPEAT 881 916 TSP TYPE-3.6.
 FT REPEAT 917 952 TSP TYPE-3.7.
 FT SITE 928 930 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 266 266 INTERCHAIN (PROBABLE).
 FT DISULFID 270 270 INTERCHAIN (PROBABLE).
 FT DISULFID 553 564 BY SIMILARITY.
 FT DISULFID 558 574 BY SIMILARITY.
 FT DISULFID 577 588 BY SIMILARITY.
 FT DISULFID 594 610 BY SIMILARITY.
 FT DISULFID 601 619 BY SIMILARITY.
 FT DISULFID 622 646 BY SIMILARITY.
 FT DISULFID 652 665 BY SIMILARITY.
 FT DISULFID 659 678 BY SIMILARITY.
 FT DISULFID 680 691 BY SIMILARITY.
 FT CARBOHYD 151 151 POTENTIAL.
 FT CARBOHYD 316 316 POTENTIAL.
 FT CARBOHYD 330 330 POTENTIAL.
 FT CARBOHYD 457 457 POTENTIAL.
 FT CARBOHYD 584 584 POTENTIAL.
 FT CARBOHYD 710 710 POTENTIAL.
 FT CARBOHYD 1069 1069 POTENTIAL.
 SQ SEQUENCE 1172 AA: 129955 MW: 2AC7BB230E44C6F5 CRC64;

Query Match 21.3%: Score 77; DB 1: Length 1172;
 Best Local Similarity 46.2%: Pred. No. 3.08e-01;
 Matches 12: Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Db 416 LGPSIOTRACSLSKDTRIRODGWS 441
 QY 46 LETSGQMRRC-VSCDCKRFEEDIDMS 70

RESULT 9
 ID YAZ1_SCHPO STANDARD: PRT: 431 AA.
 AC Q10223;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHETICAL 49.6 KD PROTEIN C13D6.01 IN CHROMOSOME 1.
 GN SPAC13D6.01.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
 OC Schizosaccharomycetaceae; Schizosaccharomyces.
 RP [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
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DR EMBL: 269725; CAA93541.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 431 AA: 49623 MW: 132FB0915646AC9F CRC64;

Query Match 20.8%: Score 75; DB 1: Length 431;
 Best Local Similarity 30.0%: Pred. No. 6.59e-01;
 Matches 12: Conservative 11; Mismatches 13; Indels 4; Gaps 4;

Db 46 FKPTQDEFEV-HCLA-RVRA-MKRLVSIQSN-FDEEDNN 81
 QY 31 FDRQVEDECKRCQMOLETSQMRRCVSCDCKRFEEDIDMS 70

RESULT 10
 ID CYSK_YEAST STANDARD: PRT: 393 AA.
 AC P53206;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE CYSTEINE SYNTHASE (EC 4.2.99.8) (O-ACETYL-SERINE
 DE SULFHYDRYLASE) (O-ACETYL-SERINE (THIO)-LYASE) (CSASE).
 GN YGR012W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RP [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE: 97435481.
 RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
 RT "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
 RT chromosome VII.";
 RL Yeast 13:1077-1090(1997).
 CC -1- CATALYTIC ACTIVITY: O-ACETYL-L-SERINE + H(2)S = L-CYSTEINE +
 CC ACETATE.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: CYSTEINE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE CYSTEINE SYNTHASE/CYSTATHIONINE BETA-
 CC SYNTHASE FAMILY.

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CC EMBL: 272797; CAA96995.1; -
 DR PROSITE: PS00901; CYS_SYNTHASE; 1.
 DR PFM; PF00291; S_T_dehydratase; 1.
 KW Hypothetical protein; Lyase; Cysteine biosynthesis;
 KW Pyridoxal phosphate.
 FT BINDING 86 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 393 AA: 42801 MW: 76C73396D7B69AC CRC64;

Query Match 20.5%: Score 74; DB 1: Length 393;
 Best Local Similarity 33.3%: Pred. No. 9.59e-01;
 Matches 13: Conservative 8; Mismatches 15; Indels 3; Gaps 3;

Db: 167 DPNQYNAAKKACNEIKKSGNIRAVFA-D-OFENEANN 203
 QY 32 DROEV-EECKRCQMOLETSQMRRCVSCDCKRFEEDIDM 69

RESULT 11
 ID TSP2_BOVIN STANDARD: PRT: 1170 AA.
 AC Q95116;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE THROMBOSPONDIN 2 PRECURSOR (CONTRACTILIN-INDUCED SECRETED PROTEIN)
 DE (CISP).

GN THBS2 OR TSP2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 CC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Danik M., Chinn A., Lefeuvre M., Keramidas M., Aquesse-Germon S.,
 RA Panhoat A., Chen H., Mosher D., Chambaz E.M., Feige J.J.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 PN [2]
 PP SEQUENCE OF 1-522 FROM N.A.
 RX MEDLINE; 96331130.
 RA Lefeuvre B., Pellerin S., Keramidas M., Danik M., Chambaz E.M.,
 RA Feige J.J.;
 RT "Opposite regulation of thrombospondin-1 and corticotropin-induced
 RT secreted protein/thrombospondin-2 expression by adrenocorticotrophic
 RT hormone in adrenocortical cells.";
 RL J. Cell. Physiol. 167:164-172(1996).
 CC -1- FUNCTION: ADHESIVE GLYCOPROTEIN THAT MEDIATES CELL-TO-CELL AND
 CC CELL-TO-MATRIX INTERACTIONS. CAN BIND TO FIBRINOGEN, FIBRONECTIN,
 CC LAMININ AND TYPE V COLLAGEN.
 CC -1- SUBUNIT: HOMOTRIMER, CROSS-LINKED BY DISULFIDE BONDS.
 CC -1- SIMILARITY: BELONGS TO THE THROMBOSPONDIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WFEC DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 3 TYPE-1 TSP REPEATS AND 7 TYPE-3 TSP REPEATS
 CC (WHICH BIND CALCIUM).
 CC -----
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 CC -----
 CC EMBL: X96540; CAA65385.1; -;
 DR PROSITE; PS00022; EGF_1; FALSE.NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01208; WFEC; 1.
 DR PFAM; PF00090; tsp-1; 3.
 DR PFAM; PF00093; wvc; 1.
 KW EGF-like domain; Cell adhesion; Calcium-binding; Heparin-binding; Repeat;
 KM EGF-like domain; Signal.
 FT CHAIN 1 18
 FT SIGNAL 1 18
 FT CHAIN 19 1170
 FT DOMAIN 19 232
 FT DOMAIN 318 375
 FT DOMAIN 379 546
 FT DOMAIN 547 690
 FT DOMAIN 723 950
 FT DOMAIN 951 1170
 FT REPEAT 379 430
 FT REPEAT 435 491
 FT REPEAT 492 546
 FT REPEAT 547 587
 FT DOMAIN 588 645
 FT DOMAIN 646 690
 FT REPEAT 723 758
 FT REPEAT 759 781
 FT REPEAT 782 817
 FT REPEAT 818 840
 FT REPEAT 841 878
 FT REPEAT 879 914
 FT REPEAT 915 950
 FT SITE 926 928
 FT DISULFID 266 266
 FT DISULFID 270 270
 FT DISULFID 551 562
 FT DISULFID 556 572
 FT DISULFID 575 586
 FT DISULFID 592 608

FT DISULFID 599 617 BY SIMILARITY.
 FT DISULFID 620 644 BY SIMILARITY.
 FT DISULFID 650 663 BY SIMILARITY.
 FT DISULFID 657 676 BY SIMILARITY.
 FT DISULFID 678 689 BY SIMILARITY.
 FT CARBOHYD 151 151 POTENTIAL.
 FT CARBOHYD 316 316 POTENTIAL.
 FT CARBOHYD 330 330 POTENTIAL.
 FT CARBOHYD 455 455 POTENTIAL.
 FT CARBOHYD 582 582 POTENTIAL.
 FT CARBOHYD 708 708 POTENTIAL.
 FT CARBOHYD 936 936 POTENTIAL.
 FT CARBOHYD 1067 1067 POTENTIAL.
 SQ SEQUENCE 1170 AA; 129862 MW; 9C1FBF55B89A051 CRC64;
 Query Match 20.5%; Score 74; DB 1; Length 1170;
 Best Local Similarity 42.3%; Pred. No. 9,59e-01;
 Matches 11; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
 DB 414 LGPSIGTRACSLGCRDHRIRODGGWS 439
 QY 46 LETSGQMRRC-VSCQDRFEEDIDWS 70
 RESULT 12
 ID EP4_HUMAN STANDARD; PRT; 125 AA.
 AC Q14508;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR (HE4) (EPIDIDYMAL
 DE SECRETOR PROTEIN E4).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISUE-EPIDIDYMIS;
 RX MEDLINE; 92153963.
 RA Kirchhoff C., Haben L., Iwell R., Krull N.;
 RT "A major human epididymis-specific cDNA encodes a protein with
 RT sequence homology to extracellular protease inhibitors.";
 RL Biol. Reprod. 45:350-357(1991).
 CC -1- FUNCTION: POSSIBLE FUNCTION IN SPERM MATURATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EPITHELIAL CELLS OF THE EPIDIDYMAL DUCT,
 CC PREDOMINANTLY WITHIN THE DISTAL SECTIONS.
 CC -1- SIMILARITY: TO WAP-TYPE 'FOUR-DISULFIDE CORE' PROTEINS.
 CC -----
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 CC -----
 CC EMBL: X63187; CAA44869.1; -;
 DR EMBL; A18924; CAA01433.1; -;
 DR HSSP; P19957; 1FLE.
 DR PROSITE; PS00317; 4-DISULFIDE-CORE; 2.
 DR PFAM; PF00095; wap; 2.
 FT SIGNAL 1 21
 FT CHAIN 22 125
 FT DOMAIN 27 75
 FT DOMAIN 76 125
 FT CARBOHYD 44 44
 SQ SEQUENCE 125 AA; 13136 MW; B5BFC08FE70E245 CRC64;
 Query Match 20.2%; Score 73; DB 1; Length 125;
 Best Local Similarity 37.5%; Pred. No. 1,39e-00;
 Matches 9; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

DB 94 CRDCCVDTQCPGOMKCRNGCCK 117
1 : : : : :
OY 39 CKROC-MOLETSGOMRCVSCQCK 61

RESULT 13
ID YORN_TTV1 STANDARD: PRT: 352 AA.

AC P19297;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-NOV-1990 (Rel. 16, Last annotation update)
OS HYPOTHEICAL 38.6 KD PROTEIN.
DE Thermoproteus tenax virus 1 (strain KRA1) (TTV1).
CC Viruses; dsDNA viruses, no RNA stage; Lipothirixviridae;
CC Lipothirixvirus.
CC [1]
RN SEQUENCE FROM N.A.

RA Neumann H.: Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: X14855; CAA32993.1; -
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 38674 MW; 0DDE49B9E08E5A88 CRC64;

Query Match 20.2%; Score 73; DB 1; Length 352;
Best Local Similarity 32.1%; Pred. No. 1.39e+00;
Matches 9; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

DB 279 NTQAFQOCISCYQ-QTSGRTQ-CINNC 304
1 : : : : :
OY 32 DROYECKRCQCMLETSQMRVCVSCQ 59

RESULT 14
ID AT11_VACCV STANDARD: PRT: 724 AA.
AC P24759;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE 94 KD A-TYPE INCLUSION PROTEIN (AT1).
OS Vaccinia virus (strain WR).
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
CC [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 91310644.
RA Amegadzie B.Y., Ahn B.-Y., Moss B.;
RT "Identification, sequence, and expression of the gene encoding a Mr
RT 35,000 subunit of the vaccinia virus DNA-dependent RNA polymerase".;
RL J. Biol. Chem. 266:13712-13718(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE: 92124754.
RA Amegadzie B.Y., Sisler J.R., Moss B.;
RT "Frame-shift mutations within the vaccinia virus A-type inclusion
RT protein gene".;
RL Virology 186:777-782(1992).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE: 92074241.
RA de Carlos A., Paes E.;
RT "Isolation and characterization of mutants of vaccinia virus with a
RT modified 94-kDa inclusion protein".;
RL Virology 185:768-778(1991).

CC -1- FUNCTION: MATURE VIRUSES ARE OCCCLUDED INTO THE ATI, AND IT HAS
CC BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING
CC DISSEMINATION FROM ANIMAL TO ANIMAL.
CC -1- MISCELLANEOUS: A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION OF
CC LARGE MASSES WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF
CC INFECTED CELLS.
CC -1- SIMILARITY: 92% IDENTITY TO COMPOX VIRUS A-TYPE INCLUSION
CC PROTEIN N-TERMINAL.
CC -----

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CC -----
DR EMBL: M61187; AAA48321.1; -
DR EMBL: M76371; AAA48275.1; -
DR EMBL: X57318; CAA40574.1; -
DR PIR: A41701; MWV294.
DR PIR: S29908; S29908.
FT CONFLICT 587 588 KO -> SK (IN REF. 3).
FT CONFLICT 610 610 R -> H (IN REF. 3).
FT CONFLICT 618 618 R -> RR (IN REF. 3).
FT CONFLICT 682 682 S -> R (IN REF. 3).
SQ SEQUENCE 724 AA; 84235 MW; C560CF61C9903028 CRC64;

Query Match 20.2%; Score 73; DB 1; Length 724;
Best Local Similarity 40.6%; Pred. No. 1.39e+00;
Matches 13; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

DB 550 KRRNVEWELS-RLRRDIECKD-YKEDIDKAR 579
1 : : : : :
OY 40 KRCQCMLETSQMRVCVSCQCKRFEEDIDMSK 71

RESULT 15
ID AT1_CAMPIC STANDARD: PRT: 726 AA.
AC 005482;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE A-TYPE INCLUSION PROTEIN (AT1).
OS Camelopox virus (strain CP-1).
CC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
CC [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 93346980.
RA Meyer H., Rziha H.-J.;
RT "Characterization of the gene encoding the A-type inclusion protein
RT of camelopox virus and sequence comparison with other
RT orthopoxviruses".;
RL J. Gen. Virol. 74:1679-1684(1993).
CC -1- FUNCTION: MATURE VIRUSES ARE OCCCLUDED INTO THE ATI, AND IT HAS
CC BEEN ASSUMED THAT SUCH BODIES PROTECT THE VIRUS DURING
CC DISSEMINATION FROM ANIMAL TO ANIMAL.
CC -1- MISCELLANEOUS: A CHARACTERISTIC FEATURE OF ATI IS THE FORMATION OF
CC LARGE MASSES WITH NO SURROUNDING MEMBRANES IN THE CYTOPLASM OF
CC INFECTED CELLS.
CC -----

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CC -----
DR EMBL: X69774; CAA49429.1; -
DR PIR: J02162; J02162.
DR PIR: S32022; S32022.

KW Late protein: Repeat. 4 X APPROXIMATE TANDEM REPEATS.
 FT DOMAIN 609 719
 FT REPEAT 609 636 1.
 FT REPEAT 637 664 2.
 FT REPEAT 665 688 3.
 FT REPEAT 689 719 4.
 SQ SEQUENCE 726 AA; 84415 MW; 1DB20A175C786F20 CRC64;

Query Match 20.2%; Score 73; DB 1; Length 726;
 Best Local Similarity 40.6%; Pred. No. 1.39e+00;
 Matches 13; Conservative 10; Mismatches 7; Indels 2; Gaps 2;

Db 551 KRRNVEWELS-RLRDIKECDK-YKEDLDKAK 580
 11: : : 1 : : : 1 : : 11 : 11 : 1 :
 QY 40 KRCOMOLETSGOMRCVSCCDKRFEEDIDWSK 71

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